

## Computer simulation to study the genetics of wild Lima bean (*Phaseolus lunatus* L.) populations.

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This study was conducted in a framework of an IBPGR project aimed at measuring the impact of the breeding system on the *in-situ* germplasm conservation for alternatively outbreeder-inbreeder species. The species, *Phaseolus lunatus*, was selected as a plant model, and the Central Valley of Costa Rica was selected as the study site due to the presence of numerous natural population of wild Lima bean (DEBOUCK, 1987). The expected outcomes are to provide further insight about genetic diversity of wild lima beans in the target area, and to settle guidelines for an *in-situ* biodiversity management.

The project started in June 1992 with two collaborating research teams, the University of San José in Costa Rica and the University of Gembloux in Belgium. The study involves four major components. A first component is the inventory, mapping and characterization of the population status in the target area. The second component is the application of methods, as isozyme electrophoresis and RAPD, to assess the genetic diversity of the populations through the area. The third component of the project concerns the setting up of field experiments to evaluate some relevant parameters of population dynamics. And the fourth component is the use of computer to integrate some mechanisms controlling the variability and the genetic structure of these populations into simulations of population genetics. This paper deals with the methodology developed for these simulation studies and their limitations.

The proposed model is typically an "individual-based model", designated also as "cellular automata" (SIGMUND, 1993); in those models the behaviour of each individual in a population is simulated separately, with its own characteristics. Such a technique is related to the models reported in literature as "stepping stone", "lattice" or "true continuum" models (KIMURA & WEISS, 1964; ROHLF & SCHNELL, 1971; SLATKIN, 1985; SLATKIN & BARTON, 1989; SOKAL & ODEN, 1978), and to the theoretical "island model" (WRIGHT, 1943). Such a simulation would have to take into account the main process suspected to perform important changes in the genetic structure of natural populations. Obviously, the multiplicity of these factors and their interactions are too complex to be ever integrated in any dynamic model. Therefore, we deliberately limited our investigations to the process in relation to the breeding system and discarded mutations and selections. Indeed, mutation effects are noticeable at a time scale which goes beyond the normal period of such a study. Concerning the selection, we have no accuracy on the way by which selective forces can act, neither their relative intensities by comparison with the genetic drift effects appearing in small populations, like those of Lima beans. Nevertheless, to reduce as much as possible differences in genetic structure among populations resulting eventually from local selective forces, a survey is being conducted in the Central Valley of San José to identify distinct homogeneous zones where *P. lunatus* populations are present.

The factors selected for simulations are: allogamy rate and its spatial distribution through the population (corresponding to the efficient pollen flow), seed dormancy, overlapping of generations, migration of genes between isolated populations, and stochastic process. In such simulations, each individual is characterized by a genotype (we consider only the monolocus case to avoid epistasis complications), its age and its location on a two-dimensional grid.

Allogamy rate and the spatial distribution of mating are notions of special interest, because there are the real crux of simulation programs. Therefore, we elaborated first a method able to adjust

automatically the allogamy rate expressed by each simulated plant according to the density and the distance with its neighboring plants. This method provides interesting results insofar as the behaviour of the system follows some observed tendencies reported in literature (sometimes amazing), in particular a diminution of outcrossing with population density (SCHAAL, 1978; SCHMITT, 1980), a potential hybrid seed production greater at intermediate distance (KLINGER, ARRIOLA, & ELLSTRAND, 1992), and differences between calculated allogamy rate depending upon the spatial distribution of the marker gene used (MOTTEN & ANTONOVICS, 1992).

A set of field experiments was launched in the Central valley of Costa Rica during April 1993 to assess the more relevant parameters involved in the population genetics. For each population, several generations will have to be studied to provide reliable results.

We have also selected four Lima bean wild populations on the basis of their isoenzymatic polymorphisms (MAQUET, 1993). Progenies of these populations will be analysed both in Gembloux (under greenhouse) and in their natural area of origin. Data obtained from the enzymatic electrophoresis will help us to test the responsiveness of the model and to adjust it according to the field observations.

Presently, we are testing simplified models developed on IBM PC compatible using "Borland Dbase IV 2.0" and "Borland Turbo C 2.0" as programming languages. These models are still simple: outcrossing occurs only between direct neighboring plants (but is density dependent), plants are annuals and there is no seed dormancy. In each generation, every individual provides "pollen" carrying marker genes that disperse according to a given spatial distribution and fertilize "ovules". In the next generation a new individual in each element is generated by choosing randomly (according to their frequencies) among the progeny produced in that grid element. Such characteristics favour a more rapid evolution than a model that considers overlapping of generations, seed dormancy and long distance pollen dispersion. The influences of the following factors are being tested: outcrossing rate, population size, initial allelic frequencies, initial genotypic frequencies, initial spatial allelic and genotypic distribution, population density and the shape of the population.

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We thank IBPGR and AGCD (Administration belge de la coopération au développement) for their support: we thank also Dr ROCHA, Dr DEBOUCK and Mr MAQUET for their collaboration.